

Figure 1

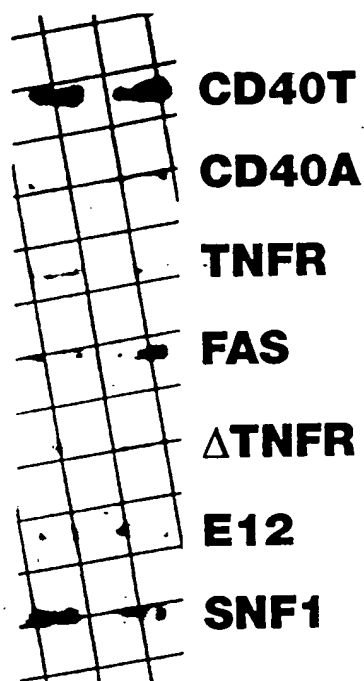


Figure 2

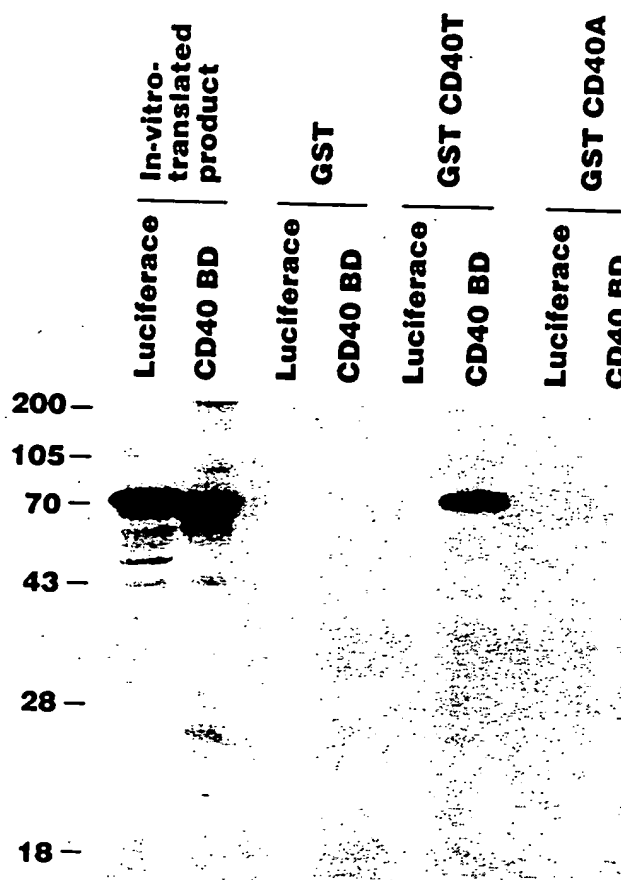


Figure 3A

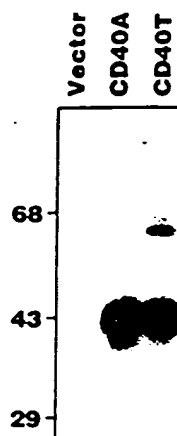


Figure 3B

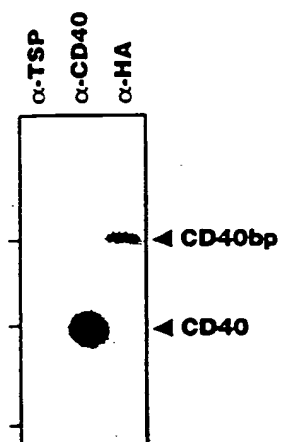


Figure 3C

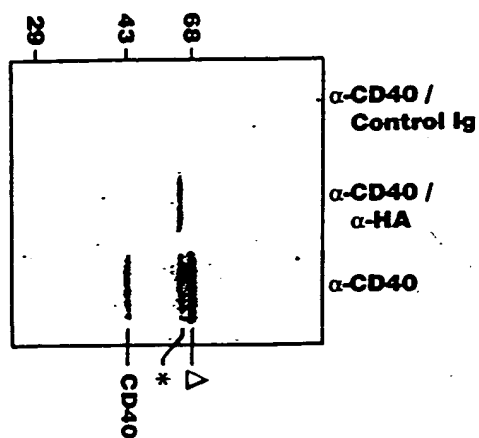


Figure 3D

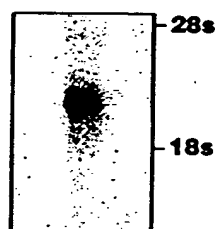
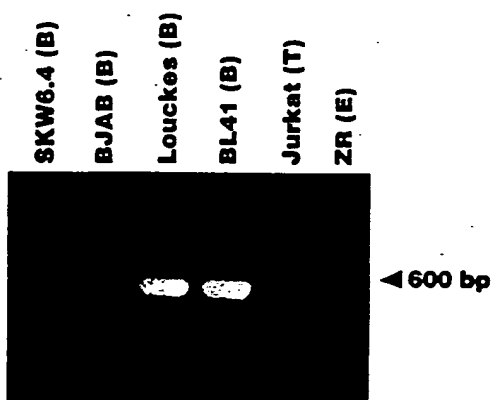


Figure 3E



MESSKKMDS PGALQTNPPLKLHTDRSAGTPVFVPEQGGYKEKFKVTVEDKYKCEK 55
 CHLVLCSPKQTECGHREFCESCMAALLSSSSPKCTACQESIIVKDKVFKDNQCKREI 110
 LALQIYCRNESRGCAEQMLGLHVLHLLKNDCHFEELPCVVRPDCKEKVLRKDLRDHV 165
 EKAÇKYREATÇSHÇKSQVPMIALQKHEDTDÇPÇVVVSÇPHKÇSVQTLRLRSELSAH 220
 LSEÇVNAPSTÇSFKRYGÇVFQGTNQIQIKAHEASSAVQHVNLLKEWNSLEKKVSL 275
 LQNESVEKNKSIQSLHNQICSEFEIEIERQKEMLRNNESEKILHLQRVIDSQAEEKLK 330
 ELDKIIRPFQRQNWEEADSMKSSVESLQNRVTELESVDKSAQVARN TGLESQLS 385
 RHDQMLSVHDIRLADMDLGFQVLETA SYNGVLIWKIRDYKRRKQEA VMGKTL SLY 440
 SQPFYTG YFGYKMCARVYLN GDMGKGCTHLSLFFVIMRGEYDALLPWPFKQKVTL 495
 MLMDQGSRRRHLGD AFKPDPNSSSFKKPTGEMN IASGCPVFVAQTVLENGTYIKD 550
 DTIFIKVIVDTS DLPDP 567

Figure 4A

49 30 289 15 12 30 23

| | | | |
|-----|---|-----|----------|
| 49 | DKYKCEKCHLVLCSPKQT-EC--GHRFCESCM AALLSSSSPKCTACQ-ESIVK | 97 | CD40bp |
| 30 | AKYLCSACKNILRRPFQA-QC--GHR YCSFCLTSILSSGPQNCAACVYEGLYE | 79 | TRAF2 |
| 289 | KSISCQICEHILADPVET-NC--KHVFCRVCI LRCLKVMGSYCPSCR-YPCFP | 337 | RAG1 |
| 15 | SELMCPICLDMLKNTMTTKEC--LHRFCSDCIVTALRSGNKECPTCR-KKLVS | 64 | RING1 |
| 12 | EEVTCPICLDPPFVEPVS I-EC--GHSFCQECISQVGKGGSVCPVCR-QRFL L | 60 | 52kd RNP |
| 30 | QAFRCHVCKDFYDSPMLT-SC--NHTFCSLCIRRC LSV-DSKCP LCR-ATDQE | 77 | UVS-2 |
| 23 | NKYTCPICFEFIYKKQIY-QCKSGHHACKECWEKSLET-KKECMTCK-SVVNS | 72 | DG17 |

Figure 4B

Figure 4C

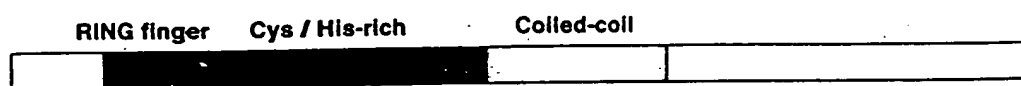
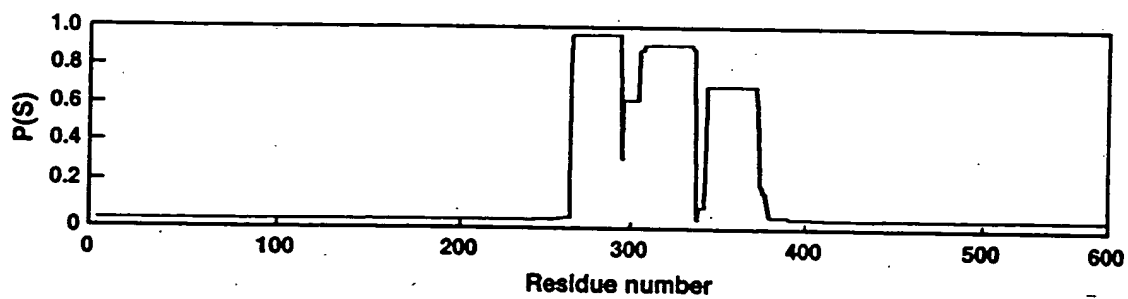


Figure 4D



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[illegible]